

GenCore version 5.1.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:10:57 ; Search time 185 Seconds  
(without alignments)  
121.126 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51

Perfect score: 51

Sequence: 1 MLQAGQCSQNEVDFSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring matrix: BLOSUM62

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 8

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	52	9 AEC02032	Amino aci
2	51	100.0	184	3 AAB08843	Amino aci
3	51	100.0	184	3 AAY94001	A human B
4	51	100.0	184	4 AAE09241	Human BCM
5	51	100.0	184	4 AAY71979	Human B c
6	51	100.0	184	4 AAB60698	Human BAF
7	51	100.0	184	4 AAE00506	Human B c
8	51	100.0	184	5 ABB81487	Human BCM
9	51	100.0	184	5 ABP54694	Metastati
10	51	100.0	184	5 AAE28961	Human B-c
11	51	100.0	184	6 AAE35216	Human B-c
12	51	100.0	184	6 ADA49361	Human BCM
13	51	100.0	184	6 ABP60552	Human tum
14	51	100.0	184	6 ABP97717	Amino aci
15	51	100.0	184	7 ADD67527	Human Lyl
16	51	100.0	184	7 ADG43715	Human B-c
17	51	100.0	184	8 ADK00756	Native hu
18	51	100.0	184	8 ADQ94442	Neutrokin
19	51	100.0	184	8 ADP56014	Human PRO
20	51	100.0	184	9 ADW03432	Human BCM
21	51	100.0	184	9 ADZ67760	Human tum
22	51	100.0	184	9 AEA23348	Tumor ant
23	51	100.0	184	9 AEC02031	Amin acid
24	51	100.0	302	4 AAB60699	Mouse IgG

25	51	100.0	302	4 AAE00507	Aae00507 Human BCM
26	51	100.0	302	7 ADG43717	Adg43717 Human B-c
27	48	94.1	51	5 AAE15485	Aae15485 Human B-c
28	48	94.1	181	5 AAE15484	Aae15484 Human B-c
29	48	94.1	184	6 ABR40082	AbR40082 Human Gen
30	48	94.1	283	5 AAE15488	Aae15488 Human BCM
31	48	94.1	288	5 ABG95060	ABg95060 Human tra
32	44	86.3	58	5 AAE15501	Aae15501 Human B c
33	40	78.4	40	9 ADZ67761	Adz67761 Human tum
34	38	74.5	38	9 AEC02033	Aec02033 Amino aci
35	34	66.7	34	5 AAE15486	Aae15486 Human B-c
36	34	66.7	34	6 ADA49366	Ada49366 Human BCM
37	29	56.9	296	9 AEC02042	Aec02042 Amino aci
38	28	54.9	34	9 AEC02025	Aec02025 Formula I
39	28	54.9	34	9 AEC02026	Aec02026 Formula I
40	28	54.9	34	9 AEC02024	Aec02024 Formula I
41	28	54.9	42	6 ABJ38417	Abj38417 TALL-1 re
42	26	51.0	26	7 ADI53060	Adi53060 Human BCM
43	19	37.3	34	9 AEC02020	Aec02020 Formula I
44	19	37.3	34	9 AEC02028	Aec02028 Formula I
45	19	37.3	34	9 AEC02017	Aec02017 Formula I

ALIGNMENTS

RESULT 1

AEC02032

ID AEC02032 standard; peptide; 52 AA.

XX AC AEC02032;

XX AC AEC02032;

DT 20-OCT-2005 (first entry)

XX DE Amino acid sequence of an extracellular domain of BCMA.

XX KW APRIL; BAFF; immune disorder; immunomodulator; antinflammatory; cancer;

XX KW cytostatic; neoplasm; immunosuppressive; therapeutic;

XX KW B-cell maturation antigen; BCMA.

XX OS Synthetic.

XX PN WO2005075511-A1.

XX PD 18-AUG-2005.

XX PF 04-AUG-2004; 2004WO-US025247.

XX PR 29-JAN-2004; 2004US-0540271P.

XX PA (GETH ) GENENTECH INC.

XX PI Kelley RF, Patel D;

XX DR WPI; 2005-555932/56.

XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful

XX PT for treating immune-related disease, cancer or T-cell mediated disease

XX PT such as graft rejection, graft versus host disease (GVHD) and

XX PT inflammation.

XX PS Disclosure; SEQ ID NO 21; 140pp; English.

XX CC The specification describes polypeptides that bind APRIL or BAFF. The

XX CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen

XX CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The

XX CC polypeptides of the invention are useful for treating immune-related

XX CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic

XX CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

XX CC sclerosis; or T-cell mediated disease such as graft rejection, graft

XX CC versus host disease (GVHD) and inflammation. The present sequence

XX CC represents an extracellular domain of BCMA.

SQ	Sequence 52 AA;	Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Query Match	100.0%; Score 51; DB 9; Length 52;					
Best Local Similarity	100.0%; Pred. No. 1.4e-47;					
Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51					
DB	1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51					
RESULT 2						
AAB08843						
ID	AAB08843 standard; peptide; 184 AA.					
XX	AC AAB08843;					
XX	02-JAN-2001 (first entry)					
DT	Amino acid sequence of human.					
DE	BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;					
KW	anti-cell death gene; apoptosis; viral infection; inflammatory response;					
KW	rheumatoid arthritis; inflammatory bowel disease; septic shock.					
XX	Homo sapiens.					
OS	Key					
XX	Location/Qualifiers					
FT	57..77					
FT	/notes "putative transmembrane domain"					
XX	WO200050633-A1.					
PN	31-AUG-2000.					
PD	24-FEB-2000; 2000WO-US004925.					
PF	24-FEB-1999; 99US-0121485P.					
PR	(GEO ) GEN HOSPITAL CORP.					
XX	Seed B, Ting A;					
PI	WPI; 2000-558405/51.					
DR	Identifying a modulator of gene expression for drug designing, by					
PT	contacting a compound library with a cell expressing an anti-cell death					
PT	gene and reporter gene, and determining alteration in reporter gene					
PT	expression.					
XX	Claim 32; Fig 7A; 53pp; English.					
PS	The present sequence represents a BCMA (not defined) polypeptide. BCMA is					
CC	a necrosis factor (NF)-kB activator. The method of the invention is used					
CC	to identify compounds which modulate BCMA activity (and thus NF-kB					
CC	activity). The specification describes a method of identifying a					
CC	polypeptide which increases gene expression from a promoter. The method					
CC	involves contacting a library of with a cell which expresses a					
CC	recombinant anti-cell death gene and a reporter gene operably linked to					
CC	the promoter, and then determining whether the expression of the reporter					
CC	gene is altered as a result of contact with library. The method is useful					
CC	for identifying polypeptides which increase or decrease gene expression					
CC	from a promoter. The BCMA polypeptide or nucleic acid are useful for					
CC	preparing a pharmaceutical composition for treating cancer, apoptosis,					
CC	viral infections, inflammatory response, such as rheumatoid arthritis,					
CC	inflammatory bowel disease or septic shock. BCMA is useful for drug					
CC	designing					
XX	Sequence 184 AA;					
Query Match	100.0%; Score 51; DB 3; Length 184;					
Best Local Similarity	100.0%; Pred. No. 4.1e-47;					
Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51					
DB	1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51					
RESULT 3						
AA94001						
ID	AA94001 standard; protein; 184 AA.					
XX	AC AAY94001;					
XX	20-OCT-2000 (first entry)					
DT	A human BCMA protein, a B cell protein related to TACI.					
DE	Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;					
KW	transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;					
KW	tnfr4 activity; antibody production; autoimmune disease; amyloidosis;					
KW	systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;					
KW	rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;					
KW	end stage renal failure; glomerulonephritis; vasculitis; nephritis;					
KW	renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;					
KW	immune response; immunosuppression; graft rejection; joint pain;					
KW	graft versus host disease; inflammation; swelling; anaemia; septic shock;					
KW	insulin dependent diabetes mellitus; Crohn's disease; hypertension;					
KW	renal artery stenosis; occlusion; cholesterol; renal emboli.					
XX	Homo sapiens.					
OS	WO200040716-A2.					
PN	13-JUL-2000.					
PD	07-JAN-2000; 2000WO-US000396.					
PF	07-JAN-1999; 99US-00226533.					
PR	(ZYMO ) ZYMOGENETICS INC.					
XX	Gross JA, Xu W, Madden K, Yee DP;					
PI	WPI; 2000-452538/39.					
DR	N-PSDB; AA58559.					
DR	Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,					
PT	renal disease, graft versus host disease, and inflammation, comprises					
PT	administering a BR43x2, TACI or BCMA extracellular domain polypeptide.					
XX	Disclosure; Page 152; 175pp; English.					
PS	The present sequence represents a human BCMA protein, a B cell protein					
CC	related to transmembrane activator and CAML-interactor (TACI) receptor.					
CC	TACI is a tumour necrosis factor (TNF) receptor. The extracellular					
CC	domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell					
CC	protein) receptor contain a cysteine rich domain, and are used for					
CC	inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used					
CC	for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated					
CC	with activated or resting B lymphocytes, effector T-cells, or with					
CC	antibody production. The antibody production is associated with an					
CC	autoimmune disease selected from systemic lupus erythematosus, myasthenia					
CC	gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity					
CC	and BR43x2, TACI or BCMA receptor-ligand engagement is associated with					
CC	asthma, bronchitis, emphysema, end stage renal failure,					
CC	glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal					
CC	neoplasms, multiple myelomas, lymphomas, light chain neuropathy,					
CC	amyloidosis, moderating immune response, immunosuppression, graft					
CC	rejection, graft versus host disease, inflammation, insulin dependent					
CC	diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or					
CC	septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,					
CC	agonists or antagonists can be used to treat hypertension, renal artery					
CC	stenosis, or occlusion, and cholesterol or renal emboli					

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XX  SQ      Sequence 184 AA;
Query Match      100.0%; Score 51; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.1e-47;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MLQWAGCQSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNCASVTNSVKG 51
    |||
Db  1  MLQWAGCQSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNCASVTNSVKG 51

RESULT 4
AAE09241
ID  ID AAE09241 standard; protein; 184 AA.
XX  AC AC
XX  AAE09241;
XX  DT 19-NOV-2001 (first entry)
XX  DE Human BCMA protein.
XX  KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
XX  KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX  KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX  OS Homo sapiens.
XX  OS
XX  PN WO200160397-A1.
XX  PN
XX  PD 23-AUG-2001.
XX  PD
XX  XX 28-NOV-2000; 2000WO-US032378.
XX  PF
XX  PR 16-FEB-2000; 2000US-0182938P.
XX  PR 22-AUG-2000; 2000US-0226986P.
XX  PR
XX  PA (GETH ) GENENTECH INC.
XX  PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX  PI Yan M;
XX  PI WPI; 2001-541628/60.
XX  DR DR
XX  DR N-PSDB; AAD15902.
XX  PT
XX  PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX  PT activity, for treating autoimmune disorders and cancer, comprises
XX  PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX  PT antagonists.
XX  PS
XX  PS Example 2; Fig 2; 160pp; English.
XX  XX
XX  CC The invention relates to methods of using one or more agonists or
XX  CC antagonists to modulate the activity of the members of TNF (tumour
XX  CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
XX  CC TACI or BCMA. The method is useful for treating pathological conditions
XX  CC or diseases associated with increased TALL-1 and APRIL expression or
XX  CC activity. TALL-1 and APRIL antagonists are used to block the interaction
XX  CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
XX  CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
XX  CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
XX  CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
XX  CC present sequence is human BCMA protein
XX  SQ      Sequence 184 AA;
Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.1e-47;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MLQWAGCQSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNCASVTNSVKG 51
    |||
Db  1  MLQWAGCQSQNEYFDSLHLHACIPQLRCSSNTPPLTCORYCNCASVTNSVKG 51

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Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 6  
 AAB60698  
 ID AAB60698 standard; protein; 184 AA.  
 AC AAB60698;  
 DT 22-MAY-2001 (first entry)  
 XX Human BAFF receptor (BAFF-R).  
 KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA;  
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
 KW renal disorder; immunosuppressive disorder; HIV infection;  
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour.  
 XX Homo sapiens.  
 OS  
 PN WO200112812-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 16-AUG-2000; 2000WO-US022507.  
 XX  
 PR 17-AUG-1999; 99US-0149378P.  
 PR 11-FEB-2000; 2000US-0181684P.  
 PR 18-FEB-2000; 2000US-0183336P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTECH R & D SA.  
 XX  
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
 PI Thompson J;  
 XX  
 XX WPI; 2001-202866/20.  
 DR N-PSDB; AAF59998.  
 XX  
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
 XX  
 XX Claim 20; Fig 1; 59pp; English.

The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia,

CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, CC autoimmune disorders and inherited B-cell-associated disorders. The CC present sequence represents human BAFF-R  
 XX  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 7  
 AAE00506  
 ID AAE00506 standard; protein; 184 AA.  
 XX  
 AC AAE00506;  
 DT 31-JUL-2001 (first entry)  
 XX Human B cell maturation protein (BCMA).  
 DE  
 XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;  
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;  
 KW tumour necrosis factor; BCMA; B cell maturation protein.  
 XX Homo sapiens.  
 OS  
 XX WO200124811-A1.  
 PN  
 PD 12-APR-2001.  
 XX  
 XX 05-OCT-2000; 2000WO-US027579.  
 PF  
 XX 06-OCT-1999; 99US-0157933P.  
 PR  
 PR 11-FEB-2000; 2000US-0181807P.  
 PR 30-JUN-2000; 2000US-0215688P.  
 XX  
 XX (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTECH R & D SA.  
 XX  
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
 PI WPI; 2001-266242/27.  
 XX  
 DR N-PSDB; AAD03844.  
 XX  
 XX Treating a mammal for a condition associated with undesired cell  
 PT proliferation such as cancer or carcinoma, comprises administering a  
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
 PT antagonist.  
 XX  
 XX Claim 3; Fig 3A; 85pp; English.

The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular

CC The present invention describes a human tumour necrosis factor receptor  
CC designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
CC antineumatic, antiarthritic, antilasthmatic, nephrotropic and hypotensive  
CC activities, and can be used in gene therapy. (I) can be used for  
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12  
CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for

CC therapeutic value  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51  
 |||||  
 RESULT 10  
 AAE28961  
 ID AAE28961 standard; protein; 184 AA.  
 XX  
 AC AAE28961;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE Human B-cell maturation antigen (BCMA).  
 XX  
 KW Human; tumour; B-cell maturation antigen; transmembrane activator;  
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;  
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;  
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;  
 KW BCMA; multiple myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..54  
 FT /note= "Antigenic epitope"  
 FT Domain 1..48  
 FT /note= "Extracellular domain"  
 FT Region 8..41  
 FT /note= "Cysteine rich region"  
 XX  
 PN WO200266516-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 XX 06-FEB-2002; 2002WO-US003500.  
 XX  
 XX 20-FEB-2001; 2001US-0270274P.  
 PR 12-APR-2001; 2001US-0283447P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA Kindevogel W;  
 XX  
 XX WPI; 2002-723183/78.  
 DR N-PSDB; AAD46410.  
 XX  
 XX B-cell maturation antigen and transmembrane activator and calcium-  
 PT modulator and cyclophilin ligand-interactor, useful for treating  
 PT disorders e.g. inflammation or lymphoma.  
 XX  
 PS Disclosure; Page 63; 67pp; English.  
 XX  
 XX The invention relates to the manufacture of a composition for inhibiting  
 CC the proliferation of tumour cells. The method involves using an antibody  
 CC component that binds both the B-cell maturation antigen (BCMA) and the  
 CC transmembrane activator and calcium-modulator and cyclophilin ligand-  
 CC interactor (TACI). BCMA and TACI binding antibody compositions are useful  
 CC for inhibiting proliferation of tumour cells, particularly inhibiting  
 CC ZTNF4 activity in a mammal associated with increased endogenous antibody  
 CC production or a disorder consisting of neoplasm, chronic lymphocytic  
 CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation  
 CC lymphoproliferative disease or light chain gammopathy or inflammation  
 CC e.g. asthma. The invention is also useful in gene therapy. The present is  
 CC human BCMA protein

XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51  
 |||||  
 RESULT 11  
 AAE35216  
 ID AAE35216 standard; protein; 184 AA.  
 XX  
 AC AAE35216;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human B-cell maturation receptor (BCMA) protein.  
 XX  
 KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
 KW B-cell maturation receptor; BCMA; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200294852-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 20-MAY-2002; 2002WO-US015910.  
 XX  
 PR 24-MAY-2001; 2001US-0293343P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA Rixon MW, Gross JA;  
 PI WPI; 2003-148455/14.  
 DR N-PSDB; AAD53754.  
 XX  
 XX Transmembrane activator and calcium modulator and cyclophilin ligand-  
 PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
 PT diabetes, comprises a TACI receptor group and an immunoglobulin group.  
 XX  
 PS Disclosure; Col 100; 71pp; English.  
 XX  
 XX The invention relates to fusion proteins comprising transmembrane  
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF2) or  
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an  
 CC immunoglobulin. The invention is used to manufacture a medicament for  
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The  
 CC composition comprising the fusion protein may also be used in treating  
 CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
 CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
 CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
 CC rejection, anaemia and septic shock. The fusion proteins are also used in  
 CC gene therapy. The present sequence is human B-cell maturation receptor  
 CC (BCMA) protein used in the invention  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 51; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Best Local Similarity	100.0%	Pred. No. 4.1e-47		Gaps	0
Matches	51	Conservative	0	Mismatches	0	Indels
1	MLWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTVNSVG	51				
1	MLWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTVNSVG	51				

RESULT 13  
ABP60552  
ID ABP60552 standard; protein; 184 AA.

AC ABP60552;  
XX  
DT 28-MAR-2003 (first entry)

28-MAR-2003 (first entry)  
Human tumour necrosis factor BCMA.

DE	Human tumour necrosis factor BCMA.
XX	APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiallergic; cytotoxic; antianemic; antiallergic; antiaesthetic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimet haemostatic; cancer; autoimmune disease; graft versus host disease; G inflammatory disorder; proliferative disorder; single chain antibody; antibody. human. BCMA: tumour necrosis factor.

OS Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

DR WPI; 2003-156740/15.

**PT** Novel isolated antibody that

PT Hodgkin's lymphoma, multiple

22

XX  
---  
XX

CC immunospecifically binds tumor

antiinflammatory, antirheumatic

CC tuberculostatic, antidiabetic

CC The antibody or its fragment

human, disease or disorder su

CC erythematosis, rheumatoid art

CC ameliorating a disease or disease

CC receptor. The disease or disc

CC asthma, allergic encephalomye-

CC system, particularly B cell c

infectious diseases (e.g. acc

10

```
CC the tumour necrosis factor BCMA
XX
SQ Sequence 184 AA;
  Query Match 100.0%; Score 51; DB 6; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||
DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||

RESULT 14
ABP97717
ID ABP97717 standard; protein; 184 AA.
XX
AC ABP97717;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human BCMA receptor.
XX
KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus; BCMA.
XX
OS Homo sapiens.
XX
PN WO2003014294-A2.
XX
PD 20-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023487.
XX
PR 03-AUG-2001; 2001US-0310114P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Dixit V, Grewal I, Ridgway J, Yan M;
XX
WPI; 2003-256560/25.
XX
DR N-PSDB; ABZ68871.
XX
PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.
XX
PS Disclosure; Fig 2; 153pp; English.
XX
The present sequence represents a human BCMA polypeptide. The
CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 184 AA;
  Query Match 100.0%; Score 51; DB 6; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||
DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||

RESULT 15
ADD67527
ID ADD67527 standard; protein; 184 AA.
XX
AC ADD67527;
XX
```

```
DT 15-JAN-2004 (first entry)
XX
DE Human Iy1732P protein SEQ ID NO:4.
XX
KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
KW vaccine; immunotherapy; cancer; multiple myeloma cell;
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003062401-A2.
XX
PD 31-JUL-2003.
XX
PF 22-JAN-2003; 2003WO-US002353.
XX
PR 22-JAN-2002; 2002US-00057475.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
PI Carter L, McNeill PD;
XX
WPI; 2003-598749/56.
XX
DR N-PSDB; ADD67526.
XX
PT New hematological malignancy-related genes and polypeptides, useful for
PT screening anti-cancer agents, and generating antibodies or
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT lymphocytic leukemia.
XX
Claim 9; SEQ ID NO 4; 307pp; English.
XX
The present invention describes an isolated polynucleotide (I), which is
CC overexpressed in haematological malignancies, and which encodes a
CC polypeptide or an immunogenic fragment of the polypeptide. Also
CC described: (1) an isolated polypeptide; (2) an expression vector
CC comprising (1) operably linked to an expression control sequence; (3) a
CC host cell comprising an expression vector; (4) an isolated antibody that
CC specifically binds to the polypeptide or its immunogenic fragment; and
CC (5) immunoconjugates comprising the antibody above, or an antibody that
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC by (i). (i) has cytostatic and immunostimulant activities, and can be
CC used in vaccines and immunotherapy. The immunoconjugates are useful in a
CC the manufacture of a medicament, particularly as active ingredients in a
CC composition for treating cancer, e.g. multiple myeloma cell, chronic
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC The polynucleotide (i) or polypeptide can be used for screening anti-
CC cancer agents, and generating antibodies or immunoconjugates for treating
CC or preventing the above-mentioned diseases. The polynucleotide,
CC polypeptide or antibody can be used for detecting, diagnosing or
CC prognosticating the haematological malignancies described above. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 184 AA;
  Query Match 100.0%; Score 51; DB 7; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||
DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTSNKG 51
  |||||

Search completed: March 2, 2006, 04:23:29
Job time : 187 secs
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:23:47 ; Search time 38 Seconds  
(without alignments)  
129.133 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51  
Perfect score: 51  
Sequence: 1 MLQAGCQSQNEFYDLSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring-table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	2 S43486	B-cell maturation
2	7	13.7	309	2 E72365	conserved hypothet
3	7	13.7	5188	2 B85547	probable RTX famil
4	7	13.7	5291	2 F90696	hypothetical prote
5	6	11.8	113	2 B72242	hypothetical prote
6	6	11.8	129	2 A81187	type IV pilin prot
7	6	11.8	148	2 B58345	myoglobin - tremet
8	6	11.8	223	2 S16652	hypothetical prote
9	6	11.8	237	2 T24407	hypothetical prote
10	6	11.8	240	2 A96697	protein FLN21.18
11	6	11.8	245	2 T36127	probable ribonucle
12	6	11.8	249	2 T45217	rec7 protein - fis
13	6	11.8	257	2 E89124	protein K07C11.1
14	6	11.8	269	2 AC0404	probable deor-fami
15	6	11.8	283	2 C86535	hypothetical prote
16	6	11.8	283	2 H72087	hypothetical prote
17	6	11.8	303	2 T17774	hypothetical prote
18	6	11.8	311	2 C69464	carboxylesterase
19	6	11.8	321	1 Q0EC15	hypothetical 34K p
20	6	11.8	321	2 F91104	hypothetical prote
21	6	11.8	321	2 A85950	hypothetical prote
22	6	11.8	327	2 S61660	probable membrane
23	6	11.8	338	2 A82209	conserved hypothet
24	6	11.8	339	2 T41126	meiotic recombinat
25	6	11.8	340	2 B96632	hypothetical prote
26	6	11.8	353	2 H75446	(S)-2-hydroxy-acid
27	6	11.8	398	1 OKBYC3	protein kinase (EC
28	6	11.8	404	2 S64944	hypothetical prote
29	6	11.8	460	2 H69095	carbon monoxide de

ALIGNMENTS

RESULT 1

S43486  
B-cell maturation factor - human  
N;Alternate names: BCM protein; BCMA protein; BEL protein  
C;Species: Homo sapiens (man)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S43486; S31208; S36661  
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
Nucleic Acids Res. 22, 1147-1154, 1994  
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidir  
A;Reference number: S43486; MUID:94218235; PMID:8165126  
A;Accession: S43486  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-184 <LA>  
A;Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:9471244; PI  
R;Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,  
EMBO J. 11, 3897-3904, 1992  
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;  
A;Reference number: S31208; MUID:93010984; PMID:1396583  
A;Accession: S31208  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-184 <LA2>  
A;Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PI  
A;Accession: S36661  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 4-184 <LA3>  
A;Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955  
C;Genetics:  
A;Gene: GDB:BCMA  
A;Cross-references: GDB:135977; OMIM:109545  
A;Map position: 16p13.1-16p13.1  
A;Introns: 44/1; 93/1  
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 51; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.6e-47;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGCQSQNEFYDLSLHAICPQLRCSNTPTPLTCQRYCNASVTNSVKG 51  
Db 1 MLQAGCQSQNEFYDLSLHAICPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 2

E72365  
conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: E72365  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

[illegible]

C:Species: Isoparorchis hypselobagri  
C:Date: 23-May-1997 #sequence\_revision 23-May-1997 #text\_change 12-Jul-2004  
C:Accession: B58345  
R:Rashid, A.R.; Van Hauwaert, M.; Haque, M.; Siddiqi, A.H.; Lasters, I.; De Mayer, M.; C  
submitted to the Protein Sequence Database, October 1996  
A:Description: Trematode myoglobins: functional molecules with a distal tyrosine.  
A:Reference number: A58345  
A:Accession: B58345  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-148 <RAS>  
A:Cross-references: UNIPROT:P80722; UNIPARC:UPI000012B54D  
A>Note: monomeric myoglobin with a tyrosine at position B10 and E7 (distal position) res  
C:Superfamily: trematode myoglobin; globin homology

Query Match 11.8%; Score 6; DB 2; Length 148;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FDSLH 19  
Db 7 FDSLH 12

RESULT 8  
S16652  
hypothetical protein\_223 - Escherichia coli retron Ec86  
C:Species: Escherichia coli retron Ec86  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 17-Jul-1998  
C:Accession: S16652  
R:Lim, D.  
Mol. Microbiol. 5, 1863-1872, 1991  
A:Title: Structure of two retrons of Escherichia coli and their common chromosomal inser  
A:Reference number: S16652; MUID:92114764; PMID:1722556  
A:Accession: S16652  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-223 <LIM>  
A:Cross-references: UNIPARC:UPI000017CAC0; EMBL:X60206  
A:Experimental source: strain B

Query Match 11.8%; Score 6; DB 2; Length 223;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRCSSN 31  
Db 152 LRCSSN 157

RESULT 9  
T24407  
hypothetical protein T03F7.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T24407  
R:Mortimore, B.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19887  
A:Accession: T24407  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-237 <WIL>  
A:Cross-references: UNIPROT:Q22118; UNIPARC:UPI00000827F9; EMBL:Z74041; PIDN:CAA98521.1;  
A:Experimental source: clone T03F7  
C:Genetics:  
A:Gene: CESP:T03F7.6  
A:Map position: 5  
A:Introns: 12/1; 53/1; 117/3; 168/3; 191/3

Query Match 11.8%; Score 6; DB 2; Length 237;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SONEYP 14  
Db 224 SONEYP 229

RESULT 10  
A96697  
protein FIN21.18 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A96697  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, A.R.; Dewar, K.  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A96697  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-240 <STO>  
A:Cross-references: UNIPROT:Q9FYF7; UNIPARC:UPI00000013F1; GB:AE005173; NID:G9828625; P  
C:Genetics:  
A:Gene: FIN21.18  
A:Map position: 1

Query Match 11.8%; Score 6; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 VTNSVK 50  
Db 142 VTNSVK 147

RESULT 11  
T36127  
probable ribonuclease PH - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T36127  
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: Z21598  
A:Accession: T36127  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-245 <SEE>  
A:Cross-references: UNIPROT:Q9S2H7; UNIPARC:UPI0000134469; EMBL:AL096852; PIDN:CAB50985  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: rph; SCORDB:SCEI9A.04c  
C:Superfamily: tRNA nucleotidyltransferase

Query Match 11.8%; Score 6; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CNASVT 46  
Db 40 CNASVT 45

RESULT 12  
T45217  
rec7 protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T45217  
R/Lin, Y.

Genetics 132, 75-85, 1992  
A/Title: Meiotically induced rec7 and rec8 Schizosaccharomyces pombe genes.

A/Reference number: Z22941; MUID:93012935; PMID:1339382

C/Accession: T45217

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-249 <LIN>

A/Cross-references: UNIPARC:UPI000017B220; EMBL:M85297; NID:gl73451; PIDN:AAA35333.1; PI

C/Genetics:

A/Gene: rec7

C/Function:

A/Description: required for meiotic intragenic recombination but not for mitotic recomb

Query Match 11.8%; Score 6; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 SNTPL 35

Db 110 SNTPL 115

RESULT 13

E89124

protein K07C11.1 [imported] - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C/Accession: E89124

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: E89124

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-257 <STO>

A/Cross-references: UNIPROT:Q21272; UNIPARC:UPI0000077A84; GB:chr\_V; PIDN:AAA96181.1; PI

C/Genetics:

A/Gene: K07C11.1

A/Map position: 5

C/Supfamily: paired box transcription factor Pax-8; paired box homology

Query Match 11.8%; Score 6; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SSNTTP 34

Db 242 SSNTTP 247

RESULT 14

AC0404

probable deoR-family regulatory protein YPO3327 [imported] - Yersinia pestis (strain CO9

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AC0404

R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-269 <KUR>

A/Cross-references: UNIPROT:Q8ZBS6; UNIPARC:UPI00000DC895; GB:AL590842; PIDN:CAC92559.1;

C/Genetics:

A/Gene: YPO3327

C/Supfamily: fuc operon regulatory protein

Query Match 11.8%; Score 6; DB 2; Length 269;

Best Local Similarity 100.0%; Pred. No. 66;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 VTNSVK 50

Db 136 VTNSVK 141

RESULT 15

C86535

hypothetical protein CPJ0357 [imported] - Chlamydophila pneumoniae (strain J138)

C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: C86535

R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie

Nucleic Acids Res. 28, 2311-2314, 2000

A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A/Reference number: A86491; MUID:20330349; PMID:10871362

A/Accession: C86535

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-283 <STO>

A/Cross-references: UNIPROT:Q9Z8I6; UNIPARC:UPI0000047124; GB:BA000008; NID:g8978729; PI

A/Experimental source: strain J138

C/Genetics:

A/Gene: CPJ0357

Query Match 11.8%; Score 6; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FDSLHL 19

Db 270 FDSLHL 275

Search completed: March 2, 2006, 04:28:14

Job time : 40 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:38:58 ; Search time 164 Seconds  
(without alignments)  
129.935 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51  
Perfect score: 51  
Sequence: 1 MLQMAQCQSQNEYFDSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table:   
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	100.0	184	4	US-10-077-438-1 Sequence 1, Appli
2	51	100.0	184	4	US-10-077-438-7 Sequence 7, Appli
3	51	100.0	184	4	US-10-077-137-1 Sequence 1, Appli
4	51	100.0	184	4	US-10-077-137-7 Sequence 7, Appli
5	51	100.0	184	4	US-10-068-725-2 Sequence 2, Appli
6	51	100.0	184	4	US-10-151-882-47 Sequence 47, Appli
7	51	100.0	184	4	US-10-115-192-8 Sequence 8, Appli
8	51	100.0	184	4	US-10-008-063-7 Sequence 7, Appli
9	51	100.0	184	4	US-10-152-363A-27 Sequence 27, Appli
10	51	100.0	184	4	US-10-216-074-11 Sequence 11, Appli
11	51	100.0	184	4	US-10-087-080-39 Sequence 39, Appli
12	51	100.0	184	4	US-10-742-634-9 Sequence 9, Appli
13	51	100.0	184	5	US-10-626-914-6 Sequence 6, Appli
14	51	100.0	184	5	US-10-485-489-6 Sequence 6, Appli
15	51	100.0	184	5	US-10-861-049-27 Sequence 27, Appli
16	51	100.0	184	5	US-10-989-826-46 Sequence 46, Appli
17	51	100.0	184	6	US-11-021-874-27 Sequence 27, Appli
18	51	100.0	302	4	US-10-115-192-12 Sequence 12, Appli
19	48	94.1	51	3	US-09-854-864-6 Sequence 6, Appli
20	48	94.1	51	3	US-09-854-864-5 Sequence 5, Appli
21	48	94.1	181	3	US-09-854-864-5 Sequence 5, Appli
22	48	94.1	181	3	US-09-855-158-5 Sequence 9, Appli
23	48	94.1	283	3	US-09-854-864-9 Sequence 9, Appli
24	48	94.1	283	3	US-09-855-158-9 Sequence 9, Appli
25	44	86.3	58	3	US-09-854-864-21 Sequence 21, Appli
26	44	86.3	58	3	US-09-855-158-21 Sequence 21, Appli
27	37	72.5	207	4	US-10-077-438-3 Sequence 3, Appli

28	37	72.5	207	4	US-10-077-137-3 Sequence 3, Appli
29	34	66.7	34	3	US-09-854-864-7 Sequence 7, Appli
30	34	66.7	34	3	US-09-855-158-7 Sequence 7, Appli
31	34	66.7	81	3	US-09-854-864-13 Sequence 13, Appli
32	34	66.7	81	3	US-09-855-158-13 Sequence 13, Appli
33	28	54.9	42	4	US-10-145-206-137 Sequence 197, App
34	10	19.6	117	3	US-09-854-864-12 Sequence 12, Appli
35	10	19.6	117	3	US-09-855-158-12 Sequence 12, Appli
36	10	19.6	185	3	US-09-854-864-11 Sequence 11, Appli
37	10	19.6	185	3	US-09-855-158-11 Sequence 11, Appli
38	10	19.6	185	4	US-10-216-074-17 Sequence 17, Appli
39	10	19.6	281	3	US-09-854-864-10 Sequence 10, Appli
40	10	19.6	281	3	US-09-855-158-10 Sequence 263362, Sequence 221552,
41	7	13.7	76	4	US-10-425-115-263362 Sequence 342318, A
42	7	13.7	84	4	US-10-424-599-221552 Sequence 73128, A
43	7	13.7	255	4	US-10-425-115-73128 Sequence 30700, A
44	7	13.7	267	4	US-10-425-114-73128
45	7	13.7	712	5	US-10-450-763-30700

ALIGNMENTS

RESULT 1  
US-10-077-438-1  
; Sequence 1, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Techopp, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Thompson, Jeffrey  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Apotech R&D S.A.  
; TITLE OF INVENTION: Baff Receptor (BCMA), An  
; FILE REFERENCE: A080PCT  
; CURRENT APPLICATION NUMBER: US/10/077,438  
; CURRENT FILING DATE: 2002-02-18  
; PRIOR APPLICATION NUMBER: 60/149,378  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/181,684  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/183,536  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-077-438-1  
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Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQMAQCQSQNEYFDSLHAACPQLRCSNTPPLTCQRYCNASVTNSVKG 51  
DB 1 MLQMAQCQSQNEYFDSLHAACPQLRCSNTPPLTCQRYCNASVTNSVKG 51  
RESULT 2  
US-10-077-438-7  
; Sequence 7, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Techopp, Jurg

```
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

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Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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RESULT 3
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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RESULT 4
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

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Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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RESULT 6

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Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

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Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSNVKG 51
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US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF594
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

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Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 51; DB 4; Length 184;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
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US-10-008-063-7
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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RESULT 11
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1el Methods of Diagnosis of Metastatic Colorectal Cancer
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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RESULT 12
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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RESULT 13
US-10-626-914-6
; Sequence 6, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHAKAPAI, ANAN
; APPLICANT: GREWAL, IQBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-6

Query Match      100.0%; Score 51; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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RESULT 14
US-10-485-489-6
; Sequence 6, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIs and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-6

Query Match      100.0%; Score 51; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEFYDLSLLHACIPQLRCSSNTPLTTCQRYCNASVTNSVKG 51  
 Db 1 MLQWAGCQSQNEFYDLSLLHACIPQLRCSSNTPLTTCQRYCNASVTNSVKG 51

RESULT 15

US-10-861-049-27  
 ; Sequence 27, Application US/10861049  
 ; Publication No. US20050095243A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andrew Chan  
 ; APPLICANT: Qian Gong  
 ; APPLICANT: Flavius Martin  
 ; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
 ; FILE REFERENCE: P2040RIUS  
 ; CURRENT APPLICATION NUMBER: US/10/861,049  
 ; CURRENT FILING DATE: 2004-06-04  
 ; PRIOR APPLICATION NUMBER: US 60/476,531  
 ; PRIOR FILING DATE: 2003-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/476,481  
 ; PRIOR FILING DATE: 2003-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/476,414  
 ; PRIOR FILING DATE: 2003-06-05  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SEQ ID NO 27  
 ; LENGTH: 184  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-861-049-27

Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.le-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEFYDLSLLHACIPQLRCSSNTPLTTCQRYCNASVTNSVKG 51  
 Db 1 MLQWAGCQSQNEFYDLSLLHACIPQLRCSSNTPLTTCQRYCNASVTNSVKG 51

Search completed: March 2, 2006, 04:42:13  
 Job time : 165 secs

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GenCore version 5.1.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 04:39:33 ; Search time 21 Seconds  
(without alignments)  
48.572 Million cell updates/sec

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Perfect score: 51  
Sequence: 1 MLQMGQCSQNEFYDSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 135339 seqs, 20000136 residues

Word size : 0

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	100.0	184	US-10-967-527A-8
3	51	100.0	184	US-11-242-294-27
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5	10	19.6	185	US-10-967-527A-10
6	7	13.7	5291	US-11-052-554A-281
7	6	11.8	231	US-11-100-183-37
8	6	11.8	313	US-11-098-686-10357
9	6	11.8	379	US-11-072-512-3298
10	6	11.8	398	US-11-132-142-7
11	6	11.8	572	US-11-072-512-3907
12	6	11.8	605	US-10-689-742-140
13	6	11.8	668	US-11-087-099-5101
14	6	11.8	766	US-10-821-234-1691
15	6	11.8	800	US-11-072-512-3534
16	6	11.8	1137	US-11-012-762-70
17	6	11.8	1461	US-11-052-554A-283
18	6	11.8	5405	US-11-108-172-1116
19	5	9.8	8	US-11-045-024-496
20	5	9.8	8	US-11-045-024-1697
21	5	9.8	8	US-11-045-024-1698
22	5	9.8	8	US-11-045-024-3636
23	5	9.8	8	US-11-045-024-4379
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25	5	9.8	8	US-11-045-024-6787

26	5	9.8	8	7	US-11-045-024-6953	Sequence 6953, Ap
27	5	9.8	8	7	US-11-045-024-7898	Sequence 7898, Ap
28	5	9.8	8	7	US-11-045-024-12102	Sequence 12102, A
29	5	9.8	8	7	US-11-045-024-12785	Sequence 12785, A
30	5	9.8	8	7	US-11-045-024-265	Sequence 265, App
31	5	9.8	8	7	US-11-045-024-643	Sequence 643, App
32	5	9.8	8	7	US-11-045-024-644	Sequence 644, App
33	5	9.8	8	7	US-11-045-024-3241	Sequence 3241, App
34	5	9.8	8	7	US-11-045-024-4503	Sequence 4503, App
35	5	9.8	8	7	US-11-045-024-6790	Sequence 6790, App
36	5	9.8	8	7	US-11-045-024-6958	Sequence 6958, App
37	5	9.8	8	7	US-11-045-024-10213	Sequence 10213, A
38	5	9.8	8	7	US-11-045-024-12084	Sequence 12084, A
39	5	9.8	8	7	US-11-045-024-13797	Sequence 13797, A
40	5	9.8	8	7	US-11-045-024-13801	Sequence 13801, A
41	5	9.8	8	7	US-11-045-024-13803	Sequence 13803, A
42	5	9.8	8	7	US-11-136-079-713	Sequence 713, App
43	5	9.8	8	7	US-11-136-079-736	Sequence 736, App
44	5	9.8	10	7	US-11-152-747-30	Sequence 30, Appl
45	5	9.8	10	7	US-11-045-024-303	Sequence 303, App

ALIGNMENTS

RESULT 1  
US-10-742-634-9  
; Sequence 9, Application US/10742634  
; Publication No. US20050249671A9  
; GENERAL INFORMATION:  
; APPLICANT: Parmelee, David  
; APPLICANT: Yeh, Ren-Hwa  
; APPLICANT: Galperina, Olga  
; APPLICANT: Hilbert, David  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses T  
; FILE REFERENCE: 1488.1810002  
; CURRENT APPLICATION NUMBER: US/10/742,634  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: US 60/435,262  
; PRIOR FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/467,198  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 9  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-742-634-9

Query Match 100.0%; Score 51; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEFYDSLHACIPQCRCSNTPLTCQRYCNASVTNSVKG 51  
Db 1 MLQMGQCSQNEFYDSLHACIPQCRCSNTPLTCQRYCNASVTNSVKG 51

RESULT 2  
US-10-967-527A-8  
; Sequence 8, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; CURRENT FILING DATE: 2004-10-18

Query Match 13.7%; Score 7; DB 7; Length 5291;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 0; Indels

QY 43 ASVTSV 49  
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Db 1814 ASVTSV 1820

## RESULT 7

US-11-100-183-37  
; Sequence 37, Application US/11100183  
; Publication No. US20050272074A1  
; GENERAL INFORMATION:  
; APPLICANT: Strategene California  
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription  
; FILE REFERENCE: 25436/2452  
; CURRENT APPLICATION NUMBER: US/11/100,183  
; PRIOR FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: US 60/559,810  
; PRIOR FILING DATE: 2004-04-06  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 37  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Bordetella pertussis  
US-11-100-183-37

Query Match 11.8%; Score 6; DB 7; Length 231;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 DSLHA 20  
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Db 118 DSLHA 123

## RESULT 8

US-11-098-686-10357  
; Sequence 10357, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10357  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-10357

Query Match 11.8%; Score 6; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ASVTSV 48  
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Db 135 ASVTSV 140

## RESULT 9

US-11-072-512-3298  
; Sequence 3298, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHICO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: 084335-0191  
; CURRENT APPLICATION NUMBER: US/11/072,512  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/350,978  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: JP 2001-379298  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3298  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-072-512-3298

Query Match 11.8%; Score 6; DB 7; Length 379;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSL 17  
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Db 163 EYFDSL 168

## RESULT 10

US-11-132-142-7  
; Sequence 7, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: 60/571,698  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Saccharomyces sp.  
US-11-132-142-7

Query Match 11.8%; Score 6; DB 7; Length 398;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CSSNTP 33  
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Db 42 CSSNTP 47

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RESULT 11
US-11-072-512-3907
; Sequence 3907, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3907
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3907

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Best Local Similarity 100.0%; Pred.No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSL 17
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Db      163 EYFDSL 168

RESULT 12
US-10-689-742-140
; Sequence 140, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-689-742-140

Query Match      11.8%; Score 6; DB 7; Length 572;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSL 17
      |||||
Db      163 EYFDSL 168

RESULT 13
US-11-087-099-5101
; Sequence 5101, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5101
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Petunia x hybrida
US-11-087-099-5101

Query Match      11.8%; Score 6; DB 7; Length 668;
Best Local Similarity 100.0%; Pred.No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 SSNTPP 34
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Db      216 SSNTPP 221

RESULT 14
US-10-821-234-1691
; Sequence 1691, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1691
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1691

Query Match      11.8%; Score 6; DB 6; Length 766;
Best Local Similarity 100.0%; Pred.No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQMAQQ 7
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Db      31 LQMAQQ 36

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US-11-072-512-3534
; Sequence 3534, Application US/11072512
; Publication No. US20060029945A1

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; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3534
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3534

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      353 QCSQNE 358

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	48	94.1	181	2	US-09-854-864-5
5	48	94.1	283	2	US-09-854-864-9
6	44	86.3	58	2	US-09-854-864-21
7	34	66.7	34	2	US-09-854-864-7
8	34	66.7	81	2	US-09-854-864-13
9	10	19.6	117	2	US-09-854-864-12
10	10	19.6	185	2	US-09-565-423-17
11	10	19.6	185	2	US-09-854-864-11
12	10	19.6	281	2	US-09-854-864-10
13	6	11.8	29	2	US-09-270-767-60339
14	6	11.8	62	2	US-09-621-976-5704
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16	6	11.8	80	2	US-09-248-796A-26829
17	6	11.8	110	2	US-09-248-796A-26879
18	6	11.8	111	2	US-09-270-767-44871
19	6	11.8	165	2	US-09-270-767-35026
20	6	11.8	165	2	US-09-270-767-50243
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22	6	11.8	179	2	US-09-252-991A-23579
23	6	11.8	197	2	US-09-248-796A-19314
24	6	11.8	201	2	US-09-134-000C-5259
25	6	11.8	233	2	US-09-248-796A-14858
26	6	11.8	237	2	US-09-543-681A-4388
27	6	11.8	270	2	US-09-543-681A-4388

28	6	11.8	291	2	US-09-198-452A-373	Sequence 373, App
29	6	11.8	291	2	US-09-438-185A-359	Sequence 359, App
30	6	11.8	297	2	US-09-902-540-15551	Sequence 15551, A
31	6	11.8	304	2	US-09-328-352-7098	Sequence 7098, Ap
32	6	11.8	311	1	US-08-602-359A-41	Sequence 41, Appl
33	6	11.8	346	2	US-09-270-767-46598	Sequence 46598, A
34	6	11.8	379	2	US-10-104-047-3298	Sequence 3298, Ap
35	6	11.8	391	2	US-09-270-767-58641	Sequence 58641, A
36	6	11.8	398	2	US-09-538-092-501	Sequence 501, App
37	6	11.8	398	2	US-09-487-558B-404	Sequence 404, App
38	6	11.8	456	2	US-09-634-238-276	Sequence 276, App
39	6	11.8	476	2	US-09-248-796A-15175	Sequence 15175, A
40	6	11.8	483	2	US-09-902-540-9827	Sequence 9827, Ap
41	6	11.8	499	2	US-08-985-492-14	Sequence 14, Appl
42	6	11.8	499	2	US-09-949-016-5906	Sequence 5906, Ap
43	6	11.8	502	2	US-09-949-016-10424	Sequence 10424, A
44	6	11.8	572	2	US-10-104-047-3907	Sequence 3907, Ap
45	6	11.8	608	2	US-09-270-767-43297	Sequence 43297, A

ALIGNMENTS

RESULT 1

US-09-565-423-11  
; Sequence 11, Application US/09565423  
; Patent No. 6475987  
; GENERAL INFORMATION:  
; APPLICANT: SRU, Hong-Bing  
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND  
; FILE REFERENCE: 2879-72  
; CURRENT APPLICATION NUMBER: US/09/565,423  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: UNKNOWN  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/132,892  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-565-423-11

Query Match 100.0%; Score 51; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-46;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWGCQSQNEFDSLLHACIPQLRCSNTPLTLCQRYCNASVTNSVKG 51  
DB 1 MLQWGCQSQNEFDSLLHACIPQLRCSNTPLTLCQRYCNASVTNSVKG 51

RESULT 2

US-09-949-016-11115  
; Sequence 11115, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11115  
; LENGTH: 192  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11115

Query Match 100.0%; Score 51; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
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DB 9 MLAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 59

## RESULT 3

US-09-854-864-6  
; Sequence 6, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-6

Query Match 94.1%; Score 48; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 7.9e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

## RESULT 4

US-09-854-864-5  
; Sequence 5, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-5

Query Match 94.1%; Score 48; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 2.3e-43;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

## RESULT 5

US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: YU, GANG  
; APPLICANT: THEILL, LARS EYDE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match 94.1%; Score 48; DB 2; Length 283;  
Best Local Similarity 100.0%; Pred. No. 3.4e-43;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

## RESULT 6

US-09-854-864-21  
; Sequence 21, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-21

Query Match 86.3%; Score 44; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.6e-39;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
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DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 44

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RESULT 7
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-7

Query Match      66.7%; Score 34; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.1e-29;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 8
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-854-864-13

Query Match      66.7%; Score 34; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.6e-29;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 9
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:

```

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; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
; US-09-854-864-12

Query Match      19.6%; Score 10; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21
DB 5 EYFDSLHAC 14

RESULT 10
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-565-423-17

Query Match      19.6%; Score 10; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21
DB 9 EYFDSLHAC 18

RESULT 11
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039

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; PRIOR FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: US 60/214,591  
 ; PRIOR FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 11  
 ; LENGTH: 185  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 US-09-854-864-11

Query Match 19.6%; Score 10; DB 2; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.0053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21  
 Db 9 EYFDSLHAC 18

RESULT 12  
 US-09-854-864-10  
 ; Sequence 10, Application US/09854864  
 ; Patent No. 6774106  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THEILL, LARS EYDE  
 ; APPLICANT: YU, GANG  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
 ; FILE REFERENCE: A-686B  
 ; CURRENT APPLICATION NUMBER: US/09/854,864  
 ; CURRENT FILING DATE: 2001-09-11  
 ; PRIOR APPLICATION NUMBER: US 60/204,039  
 ; PRIOR FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: US 60/214,591  
 ; PRIOR FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 281  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-854-864-10

Query Match 19.6%; Score 10; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.0075;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21  
 Db 9 EYFDSLHAC 18

RESULT 13  
 US-09-270-767-60339  
 ; Sequence 60339, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 60339  
 ; LENGTH: 29  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 US-09-270-767-60339

Query Match 11.8%; Score 6; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRCSSN 31  
 Db 2 LRCSSN 7

RESULT 14  
 US-09-621-976-5704  
 ; Sequence 5704, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 5704  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: -43..-1  
 US-09-621-976-5704

Query Match 11.8%; Score 6; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CSSNTP 33  
 Db 49 CSSNTP 54

RESULT 15  
 US-09-510-252-2  
 ; Sequence 2, Application US/09510252  
 ; Patent No. 6372490  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandabalan, Krishnan  
 ; APPLICANT: Yang, Meijia  
 ; APPLICANT: Schulz, Vincent  
 ; APPLICANT: Curagen Corporation  
 ; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
 ; FILE REFERENCE: 15966-524 MDM US  
 ; CURRENT APPLICATION NUMBER: US/09/510,252  
 ; CURRENT FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: USSN 60/121,192  
 ; PRIOR FILING DATE: 1999-02-23  
 ; PRIOR APPLICATION NUMBER: USSN 60/122,643  
 ; PRIOR FILING DATE: 1999-03-03  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 74  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Any X can be any amino acid.  
 US-09-510-252-2

Query Match 11.8%; Score 6; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 COLRCS 29

Db 44 CQRCs 49

Search completed: March 2, 2006, 04:29:06  
Job time : 47 secs

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3	10	19.6	185	1	TNR17_MOUSE	Q88472 mus musculu
4	8	15.7	148	2	Q5UK76_ORISA	Q5JK76 oryza sativ
5	8	15.7	499	2	Q88714_MOUSE	Q88714 mus musculu
6	8	15.7	1674	2	Q80Z18_MOUSE	Q80Z18 mus musculu
7	8	15.7	2850	2	Q80T03_MOUSE	Q80T03 mus musculu
8	7	13.7	140	2	Q800M3_MORAM	Q800m3 morone amer
9	7	13.7	140	2	Q800M4_MORCH	Q800m4 morone chry
10	7	13.7	140	2	Q800M5_MORCS	Q800m5 morone chry
11	7	13.7	140	2	Q800M6_MORSA	Q800m6 morone saxa
12	7	13.7	175	2	Q8BHX4_MOUSE	Q8BHX4 mus musculu
13	7	13.7	202	2	Q9JDU3_9H1V1	Q9JDU3 human immu
14	7	13.7	206	2	Q8LX76_9D1PT	Q8LX76 chaoborus a
15	7	13.7	207	2	Q8AS74_9H1V1	Q8as74 human immu
16	7	13.7	258	2	Q8BHS1_MOUSE	Q8bhs1 mus musculu
17	7	13.7	264	2	Q4YHA8_PLABE	Q4Yha8 plasmodium
18	7	13.7	307	2	Q4YZ16_PLABE	Q4yz16 plasmodium
19	7	13.7	307	2	Q5DIB6_EPICO	Q5dib6 epinephelus
20	7	13.7	309	2	Q9WYV9_THEMA	Q9wyv9 thermotoga
21	7	13.7	333	2	Q67H7F_9V1RU	Q67hf3 lymphocyati
22	7	13.7	385	2	Q6MT77_MYCMS	Q6mt77 mycoplasma
23	7	13.7	409	2	Q67ZQ5_9H1V1	Q67zq5 human immu
24	7	13.7	411	2	Q5FW06_XENTR	Q5fw06 xenopus tro
25	7	13.7	412	2	Q5U4G6_MOUSE	Q5u4g6 mus musculu
26	7	13.7	412	2	Q8K3A5_MOUSE	Q8k3a5 mus musculu
27	7	13.7	412	2	Q8BHQ2_MOUSE	Q8bhq2 mus musculu
28	7	13.7	413	2	Q4HZP5_GIBZE	Q4hzp5 gibberella
29	7	13.7	457	2	Q8AVS9_XENLA	Q8avs9 xenopus lae
30	7	13.7	804	2	Q8WRL8_TETTH	Q8wrl8 tetrahymena
31	7	13.7	945	2	O52P58_MAC3R	O52f58 magnaporthe

RA Sherwood J.K., Sherwood A.M., Leitchauer B.J., Nickerson D.A.;  
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department  
of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.  
RX MEDLINE=20363816; PubMed=10903733;  
RA Hatogai A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,  
RA Inoue J.-I., Devergne O., Tsapis A.;  
RT "TNF receptor family member BCMA (B cell maturation) associates with  
TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and  
activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-  
activated protein kinase.";  
RN Immunol. 165:1322-1330(2000).  
RP FUNCTION.  
RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;  
Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,  
Madden K., Xu W., Parikh-Novak J., Foster D., Lofton-Day C.,  
Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,  
Harrison K., Kindsvogel W., Clegg C.H.;  
RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell  
autoimmune disease.";  
RN Nature 404:995-999(2000).  
RP FUNCTION.  
RX MEDLINE=20170294; PubMed=10973284; DOI=10.1038/79802;  
Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,  
McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;  
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating  
humoral immunity.";  
RN Nat. Immunol. 1:252-256(2000).  
RP INTERACTIONS WITH TRAF5 AND TRAF6.  
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
Shu H.-B., Johnson H.;  
RT "B cell maturation protein is a receptor for the tumor necrosis factor  
family member TALL-1.";  
RN Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).  
CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.  
CC Promotes B-cell survival and plays a role in the regulation of  
humoral immunity. Activates NF-kappa-B and JNK.  
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC -!- INTERACTION:  
CC Q9Y275:TNFSF13B; NbExp-1; IntAct=EBI-519945; EBI-519169;  
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane  
and perinuclear Golgi-like structures.  
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-  
cells or monocytes.  
CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a  
form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation  
t(4;16)(q26;pl3) with IL2.  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC  
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between the Swiss Institute of Bioinformatics and the EMBL outstation  
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use as long as its content is in no way modified and this statement is not  
removed.  
CC  
CC EMBL; Z14954; CAA78679.1; -; mRNA.  
CC EMBL; Z29575; CAAB2691.1; -; mRNA.  
CC EMBL; Z29574; CAAB2690.1; -; Genomic DNA.  
CC EMBL; U95742; AAB67251.1; -; Genomic DNA.  
CC EMBL; AB052772; BAB60895.1; -; Genomic DNA.  
CC EMBL; AY509112; AAR84240.1; -; Genomic DNA.  
CC F03; S43486; S43486.  
CC PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.  
CC PDB; 1XU2; X-ray; R/S/T=5-51.  
CC IntAct; Q02223; -;  
CC Ensembl; ENSG00000048462; Homo sapiens.  
CC HGNC; HGNC:11913; TNFRSF17.

DR MIM; 109545; -;  
DR GO; GO:0016021; C: integral to membrane; TAS.  
DR GO; GO:0005886; C: plasma membrane; TAS.  
DR GO; GO:0004872; P: receptor activity; TAS.  
DR GO; GO:0008283; P: cell proliferation; TAS.  
DR GO; GO:0007275; P: development; TAS.  
DR GO; GO:0007145; P: signal transduction; TAS.  
DR InterPro; IPR001368; TNFR\_C6.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE NEG.  
KW 3D-structure; Chromosomal translocation; Immune response;  
KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.  
FT TOPO\_DOM 1 54 Extracellular (Potential)  
FT TRANSMEM 55 77 Signal-anchor for type III membrane  
FT protein (Potential).  
FT TOPO\_DOM 78 184 Cytoplasmic (Potential).  
FT REPEAT 7 41 TNFR-Cys.  
FT SITE 3 4 Breakpoint for translocation to form  
FT IL2/TNFRSF17 oncogene.  
FT DISULFID 8 21 By similarity.  
FT DISULFID 24 37 By similarity.  
FT DISULFID 28 41 By similarity.  
FT VARIANT 54 54 A -> V.  
FT VARIANT 65 65 /FTid=VAR\_018755.  
FT VARIANT 75 75 I -> V.  
FT VARIANT 81 81 /FTid=VAR\_018756.  
FT VARIANT 153 153 S -> N (in dbSNP:373496).  
FT VARIANT 165 165 A -> T.  
FT VARIANT 165 165 /FTid=VAR\_012234.  
FT VARIANT 165 165 C -> S.  
FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;  
SQ  
Query Match 100.0%; Score 51; DB 1; Length 184;  
Best Local Similarity 100.0%; Pred. No. 3.4e-47;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQWAGQCSQNEYFDSLHACIPQLCRSSNTPPLTCORYCNASVTNSVKG 51  
DB 1 MLQWAGQCSQNEYFDSLHACIPQLCRSSNTPPLTCORYCNASVTNSVKG 51  
RESULT 2  
QSP646 HUMAN  
ID Q6PE46\_HUMAN PRELIMINARY; PRT; 184 AA.  
AC Q6PE46;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Tumor necrosis factor receptor superfamily, member 17.  
GN Name=TNFRSF17;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Poolled;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Poolled;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; SC058291; AAHS291.1; -; mRNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;  
 Query Match 100.0%; Score 51; DB 2; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-47; Indels 0; Gaps 0;  
 Matches 51; Conservative 0; Mismatches 0;  
 OY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSYK 51  
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSYK 51  
 RESULT 3  
 TNRL7 MOUSE  
 ID TNRL7 MOUSE STANDARD; PRT; 185 AA.  
 AC 088472;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell  
 maturation protein).  
 DE Name=TNFRsf17; Synonyms=Bcm, Bcma;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).  
 RC STRAIN=BALB/c; TISSUE=Spleen;  
 RX MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;  
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,  
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.  
 RT "The characterization of murine BCMA gene defines it as a new member  
 of the tumor necrosis factor receptor superfamily."  
 RL Int. Immunol. 10:1693-1702(1998).  
 [2]  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziera R.M., King B.L.,  
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshak-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 [3]  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.A., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Receptor for TNFSF13B/Blys/BAFF and TNFSF13/APRIL.  
 CC Promotes B-cell survival and plays a role in the regulation of  
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).  
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O88472-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O88472-2; Sequence=VSP\_006507;  
 CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and  
 CC heart, and at lower levels in kidney and lung.  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AF061505; AAC23799.1; -; mRNA.  
 CC EMBL; AK020247; BAB32038.1; -; mRNA.  
 CC EMBL; BC027519; AAH27519.1; -; mRNA.  
 CC HSSP; 002223; LOOP.  
 CC Ensembl; ENSMUSG00000022496; Mus musculus.  
 CC MGI; MGI:1343050; Tnfrsf17.  
 CC GO; GO:0016021; C:integral to membrane; TAS.  
 CC InterPro; IPR001368; TNFR\_C6.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
 CC PROSITE; PS00505; TNFR\_NGFR\_2; FALSE NEG.  
 CC Alternative splicing; Immune response; Receptor; Signal-anchor;  
 CC Transmembrane.  
 CC TOPO DOM 1 49 Extracellular (Potential).  
 CC TRANSMEM 50 70 Signal-anchor for type III membrane

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FT TORO_DOM 71 185 protein (Potential).
FT REPEAT 4 36 Cytoplasmic (Potential).
FT DISULFID 5 18 TNFR-Cys.
FT DISULFID 21 32 By similarity.
FT DISULFID 25 36 By similarity.
FT VARSPLIC 87 91 Missing (in isoform 2).
FT /FTId=VSP_006507.
SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 19.6%; Score 10; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EYFDSLHAC 21
Db 9 EYFDSLHAC 18

RESULT 4
ID Q5JK76 OLYSA PRELIMINARY; PRT; 148 AA.
AC Q5JK76;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein OSUNBA0024F24.16 (Hypothetical protein
DE B1156H12.31).
GN Name=OSJNBa0024F24.16; Synonyms=B1156H12.31;
OS Oryza sativa (japonica cultivar-group)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP004258; BAD88121.1; -; Genomic DNA.
DR EMBL; AP004225; BAD88061.1; -; Genomic DNA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16215 MW; DB06C14D76E647CE CRC64;

Query Match 15.7%; Score 8; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 SILHACIP 23
Db 135 SILHACIP 142

RESULT 5
ID O88714 MOUSE PRELIMINARY; PRT; 499 AA.
AC O88714;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gastric mucin-like protein (Fragment).
GN Name=Muc6; Synonyms=gasttric mucin-like;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tomasetto C.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -; mRNA.
DR HSSP; P56682; ICCV.
DR Ensembl; ENSMUSG00000048191; Mus musculus.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00216; VWD; 1.
DR NON_TER 1
FT NON_TER 499
FT SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 15.7%; Score 8; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFD 15
Db 430 CSQNEYFD 437

RESULT 6
ID Q80Z18 MOUSE PRELIMINARY; PRT; 1674 AA.
AC Q80Z18;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted gel-forming mucin (Fragment).
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RC PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
RA Escande F., Buisine M.P.;
RT "The mouse secreted gel-forming mucin gene cluster.";
RL Biochim. Biophys. Acta 1676:240-250(2004).
DR EMBL; AJ511867; CAD54415.1; -; Genomic DNA.
DR EMBL; AJ511868; CAD54415.1; JOINED; Genomic DNA.
DR HSSP; O46162; 1KJ0.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR NON_TER 1674
FT NON_TER 1674

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SQ SEQUENCE 1674 AA; 181168 MW; 3BC42CB004476309 CRC64;
Query Match 15.7%; Score 8; DB 2; Length 1674;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFD 15
DB 1181 CSQNEYFD 1188

RESULT 7
Q80T03 MOUSE
ID Q80T03_MOUSE PRELIMINARY; PRT; 2850 AA.
AC Q80T03;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MUC6.
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J;
RC MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0898-7543(03)00036-3;
RA Desseyn J.-L., Laine A.;
RT "Characterization of mouse muc6 and evidence of conservation of the
RT gel-forming mucin gene cluster between human and mouse.";
RL Genomics 81:433-436(2003).
DR EMBL; AY184388; AAC47735.1; -; Genomic_DNA.
DR EMBL; AY184385; AAC47735.1; JOINED; Genomic_DNA.
DR EMBL; AY184387; AAC47735.1; JOINED; Genomic_DNA.
DR EMBL; AY184386; AAC47735.1; JOINED; Genomic_DNA.
DR HSSP; O46162; 1KJ0
DR Ensembl; ENSMUSG0000048191; Mus musculus.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK 2; 1.
SQ SEQUENCE 2850 AA; 300398 MW; 9CD95F0845C79C9D CRC64;
Query Match 15.7%; Score 8; DB 2; Length 2850;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFD 15
DB 1222 CSQNEYFD 1229

RESULT 8
Q800M3 MORAM
ID Q800M3_MORAM PRELIMINARY; PRT; 140 AA.
AC Q800M3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Morone americana (White perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OC NCBI_TaxID=46260;
RN [1]
NUCLEOTIDE SEQUENCE.
RP Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Plays a key role in the control of the eukaryotic cell
cycle. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
MPF (By similarity).
-!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
mature oocytes (By similarity).
EMBL; AF402675; AAC73860.1; -; mRNA.
HSSP; P08069; 1JQH.
SMR; Q800M4; 1-140.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;
Query Match 13.7%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQ 7
DB 103 MLQMAQ 109

RESULT 9
Q800M4 MORCH
ID Q800M4_MORCH PRELIMINARY; PRT; 140 AA.
AC Q800M4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Morone chrysops (White bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OC NCBI_TaxID=46259;
RN [1]
NUCLEOTIDE SEQUENCE.
RP Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Plays a key role in the control of the eukaryotic cell
cycle. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
MPF (By similarity).
-!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
mature oocytes (By similarity).
EMBL; AF402675; AAC73860.1; -; mRNA.
HSSP; P08069; 1JQH.
SMR; Q800M4; 1-140.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
```

DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008286; Tyr\_kinase\_AS.  
 DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Receptor.

FT NON\_TER 1 1  
 FT NON\_TER 140 140

SQ SEQUENCE 140 AA; 15815 MW; AC3C1C98A1674D1B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7  
 |||||  
 Db 103 MLQMAQG 109

# RESULT 10

Q800M5 MORCS PRELIMINARY; PRT; 140 AA.

AC Q800M5; 1-140.

DT 01-JUN-2003 (TREMELrel. 24, Created)

DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE Insulin-like growth factor I receptor (Fragment).

OS Morone chrysops x Morone saxatilis (White bass x Striped bass).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;

OC Moronidae; Morone.

OX NCBI\_TaxID=45352;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Fruchtmann S., Hawkins M.B., Borski R.J.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell

cycle. It is required in higher cells for entry into S-phase and

mitosis. Component of the kinase complex that phosphorylates the

repetitive C-terminus of RNA polymerase II. Catalytic component of

MPF (By similarity).

CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in

mature oocytes (By similarity).

CC EMBL; AF402674; AAC73859.1; -; mRNA.

DR HSSP; P08069; IJOH.

DR SMR; Q800M5; 1-140.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR001245; Tyr\_kinase.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

KW Receptor.

FT NON\_TER 1 1

FT NON\_TER 140 140

SQ SEQUENCE 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7  
 |||||  
 Db 103 MLQMAQG 109

## RESULT 11

Q800M6 MORSA PRELIMINARY; PRT; 140 AA.

AC Q800M6; 1-140.

DT 01-JUN-2003 (TREMELrel. 24, Created)

DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE Insulin-like growth factor I receptor (Fragment).

OS Morone saxatilis (Striped bass).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;

OC Moronidae; Morone.

OX NCBI\_TaxID=34816;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Fruchtmann S., Hawkins M.B., Borski R.J.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell

cycle. It is required in higher cells for entry into S-phase and

mitosis. Component of the kinase complex that phosphorylates the

repetitive C-terminus of RNA polymerase II. Catalytic component of

MPF (By similarity).

CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in

mature oocytes (By similarity).

CC EMBL; AF402673; AAC73858.1; -; mRNA.

DR HSSP; P08069; IJOH.

DR SMR; Q800M6; 1-140.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR001245; Tyr\_kinase.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

KW Receptor.

FT NON\_TER 1 1

FT NON\_TER 140 140

SQ SEQUENCE 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7  
 |||||

Db 103 MLQMAQG 109

## RESULT 12

Q8BHX4 MOUSE

ID Q8BHX4 MOUSE PRELIMINARY; PRT; 175 AA.

AC Q8BHX4;

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched

library, clone:4831418F03 product:HYPOTHETICAL 28.4 kDa PROTEIN

DE homolog (Fragment).

GN Name=Wdr32; Synonyms=AA959934;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.



```
OS Chaoborus americanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Chaoboridae;
OC Chaoborus.
OX NCBI_TaxID=204565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Berendonk T.U.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427618; CAD44504.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23927 MW; E6BC8651E8AE571 CRC64;

Query Match 13.7%; Score 7; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SSNTPEL 35
DB 137 SSNTPEL 143

RESULT 15
Q8AS74 9HIV1
ID Q8AS74_9HIV1 PRELIMINARY; PRT; 207 AA.
AC Q8AS74_
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
GS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Frey S., Gupta P., Learn G.H., Mittler J., Shriner D.,
RA Nickle D.C., Jensen M.A., Rodrigo A.G., Beerli P., He X., Zhao H.,
RA Rossini A., Felsenstein J., Walker B.D., Mullins J.I.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF535413; AAN07372.1; -; Genomic_RNA.
DR SMR; Q8AS74; 1-207.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22946 MW; DCD2182D0A73F90B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 QLRCSN 31
DB 174 QLRCSN 180

Search completed: March 2, 2006, 04:27:30
Job time : 237 secs
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